

TECH CENTER 1600/2900

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500

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RAW SEQUENCE LISTING DATE: 12/13/2001
PATENT APPLICATION: US/09/589,870B TIME: 13:38:12

Input Set : A:\547.app.txt
Output Set: N:\CRF3\12132001\I589870B.raw

4 <110> APPLICANT: Goshorn, Stephen C.
5 Graves, Scott Stoll
6 Schultz, Joanne Elaine
7 Lin, Yakang
8 Sanderson, James A.
9 Reno, Jonh M.
11 <120> TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
12 METHODS OF USE THEREOF
15 <130> FILE REFERENCE: 690022.547
17 <140> CURRENT APPLICATION NUMBER: US 09/589,870B
C--> 18 <141> CURRENT FILING DATE: 2001-11-30
20 <160> NUMBER OF SEQ ID NOS: 47
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 638
26 <212> TYPE: DNA
27 <213> ORGANISM: Streptomyces avidinii
29 <400> SEQUENCE: 1
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31 cgtcggtgca gccatcgccg tttccctgac cacggctctcg attacggcca gcgcttcggc
32 agaccctcc aaggactcga aggcccaggt ctggccgcc gaggccggca tcaccggcac
33 ctggtacaac cagctcggtcgac cgtgaccgcg ggcggccgacg ggcggccgtac
34 cggaacctac gagtcggccg tcggcaacgcg cgagagccgc tacgtcctga cgggtcggtta
35 cgacagcgcc cggccaccc acggcagcgg caccggccctc gttggacgg tgccctggaa
36 gaataactac cgcaacgccc actccgcgac cacgtggagc ggccagtacg tcggccggcgc
37 cgaggcgagg atcaacacccc agtgggtgct gacccgcgaccaccggagg ccaacgcgtc
38 gaagtccacg ctggtcggcc acgacaccc ttccaaagggtg aagccgtccg cccctccat
39 cgacgcccgg aagaaggccg gcgtcaacaa cggcaaccccg ctcgacgccc ttcagcagta
40 gtcgcgtccc ggcacccggcg ggtgcgggaa cctcgcc
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 183
44 <212> TYPE: PRT
45 <213> ORGANISM: Streptomyces avidinii
47 <400> SEQUENCE: 2
48 Met Arg Lys Ile Val Val Ala Ala Ile Ala Val Ser Leu Thr Thr Val
49 1 5 10 15
50 Ser Ile Thr Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala
51 20 25 30
52 Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln
53 35 40 45
54 Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr
55 50 55 60
56 Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu
57 65 70 75 80
58 Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala
59 85 90 95
60 Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser

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61	100	105	110
62	Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile		
63	115	120	125
64	Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp		
65	130	135	140
66	Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser		
67	145	150	155
68	Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly Val Asn Asn Gly Asn		
69	165	170	175
70	Pro Leu Asp Ala Val Gln Gln		
71	180		
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74	<211> LENGTH: 1612		
75	<212> TYPE: DNA		
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81	ccatcgaccc ggacctcgac catccagtgc tgccgc当地 gacacatgcc gcactgctgt	180	
82	ttgttcaccc acaccgtcgtg tgcacggcc gaggtcacaac accttgcacgg gcgggataacg	240	
83	gacggcgcac gccacagcgc gccctccgtc cccgc当地ggc aacaactagg gagtattttt	300	
84	cgtgtctcac atgcgaaga tcgtcggtgc agccatcgcc gtttccctga ccacggcttc	360	
85	gattacggcc atggctgaca tccagatgac tcagtcctca tcgtccttgt ctgcctctgt	420	
86	gggagacaga gtcacgatca ctgtcgccc tagtcaggc attagaggta atttagactg	480	
87	gtatcagcag aaacctggta agggaccgaa actcctaatac tactccacat ccaatttaaa	540	
88	ttctgggtgc ccatcaaggt tcagtggcag tgggtctggg tcagattata ctctcaccat	600	
89	cagcagcctt cagcctgaag atttcgcaac gtattactgt ctacagcgtt atgcgtatcc	660	
90	gtacacgttc ggacaaggga ccaagctgga gatcaagatc tctggc当地ggc gtggctc当地gg	720	
91	cgggtggc当地 tcgggtggc当地 gaggctcgag ccaggttcag ctggccagtg ctggggcaga	780	
92	ggtaaaaaag ccaggggcct cagtcaaggt gtcctc当地aa gcttctggc当地 tcaacattaa	840	
93	agacacatat atgcactggg tgagggcaggc acctggacag ggcctc当地agtg ggatggaaag	900	
94	gattgatcct gc当地aatggta atactaaatc cgacctgtcc ttccaggc当地 gggactat	960	
95	aacagcagac acgtccatca acacagccta catggaaactc agcagcctga ggtctgacga	1020	
96	cactgccgtc tattactgtt cttagagaggt cctaactggg acgtggctt tggactactg	1080	
97	gggtcaagga accttagtca cc当地tgc当地ctc tggctctggc当地 tggc当地agacc cctcc当地agga	1140	
98	ctc当地aggcc caggctc当地 cc当地ggc当地aggc cggcatcacc ggc当地ctggc当地 acaaccagct	1200	
99	cggtctgacc tt当地atc当地tgc当地 cc当地ggg当地ggc当地 cgacggcc当地 ctgaccggaa cctacgagtc	1260	
100	ggccgtc当地ggc当地 aacgccc当地gaga gccgctacgt cctgaccggc当地 cggtacgaca gc当地ccccggc当地	1320	
101	caccgacggc当地 agcggc当地accgg cc当地tgc当地ttg gacggtggcc当地 tgg当地agaata actaccgca	1380	
102	cgccc当地actcc ggc当地accacgt ggagggcc当地 gtacgtc当地ggc当地 ggcc当地ggagg cgaggatcaa	1440	
103	cacccactgg ctgctgaccc cccgacccac cgaggcc当地 acctggaaatg ccacgctgg	1500	
104	cgccacgac accttc当地acca aggtgaagcc gtccgccc当地 tccatc当地gacg cggc当地agaa	1560	
105	ggccggc当地tc当地 aacaacggc当地 accccgctc当地 ga cggcc当地ttc当地ag cagtaaggat cc	1612	
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108	<211> LENGTH: 431		
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112	<400> SEQUENCE: 4		
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Input Set : A:\547.app.txt
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114	1	5	10	15
115	Ser Ile Thr Ala Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser			
116	20	25	30	
117	Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser			
118	35	40	45	
119	Gln Gly Ile Arg Gly Asn Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys			
120	50	55	60	
121	Gly Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val			
122	65	70	75	80
123	Pro Ser Arg Phe Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr			
124	85	90	95	
125	Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln			
126	100	105	110	
127	Arg Asn Ala Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile			
128	115	120	125	
129	Lys Ile Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly			
130	130	135	140	
131	Gly Ser Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
132	145	150	155	160
133	Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile			
134	165	170	175	
135	Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
136	180	185	190	
137	Gln Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Ser Asp			
138	195	200	205	
139	Leu Ser Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ile Asn			
140	210	215	220	
141	Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val			
142	225	230	235	240
143	Tyr Tyr Cys Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr			
144	245	250	255	
145	Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Ser Ala			
146	260	265	270	
147	Asp Pro Ser Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly			
148	275	280	285	
149	Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr			
150	290	295	300	
151	Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly			
152	305	310	315	320
153	Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro			
154	325	330	335	
155	Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys			
156	340	345	350	
157	Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr			
158	355	360	365	
159	Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser			
160	370	375	380	
161	Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp			
162	385	390	395	400

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163 Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys
 164 405 410 415
 165 Lys Ala Gly Val Asn Asn Gly Asn Pro Leu Asp Ala Val Gln Gln
 166 420 425 430
 168 <210> SEQ ID NO: 5
 169 <211> LENGTH: 1239
 170 <212> TYPE: DNA
 171 <213> ORGANISM: Streptomyces avidinii
 173 <400> SEQUENCE: 5
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 175 atgacttgca gggccagctc aagttaagt tacatgcact ggtaccagca gaagccagga 120
 176 tcctccccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 180
 177 ttcagtggca gtgggtctgg gacctttagt tcttcacaa tcagcagagt ggaggctgaa 240
 178 gatgctgcca cttattactg ccagcagttgg attagtaacc caccacacgtt cgggtctgg 300
 179 accaagctgg agctgaagat ctctggctg gaaggcagcc cggaagcagg tctgtctcg 360
 180 gacgcaggtt ccggctcgag ccaggttcaag ctgggtccagt caggggctga gctggtaag 420
 181 cctggggcct cagtgaagat gtcctgcaag gcttctggct acacattiac cagttacaat 480
 182 atgcactggg taaagcagac acctggacag ggcctggaaat ggattggagc tatttatcca 540
 183 gaaaaatggtg atacttccta caatcagaag ttcaaaggca aggccacatt gactgcagac 600
 184 aaatcctcca gcacagccta catgcagctc agcagcctga catctgagga ctctgcggc 660
 185 tattactgtg caagagcgca attacgacat aactactggt acttcgatgt ctggggcgca 720
 186 gggaccacagg tcaccgtgag ctctggctc ggttggcag acccctccaa ggactcgaag 780
 187 gcccaggctc cggccgcccga ggcggcgtc accggcacct ggtacaacca gtcggctcg 840
 188 accttcatcg tgaccggcgg cggcgcacgc gccctgaccg gAACCTACGA gtcggccgtc 900
 189 ggcaacgccc agagccgcta cgtcctgacc ggtcggtacg acagcgcggc ggcaccgac 960
 190 ggcagcggca cgcgcctcgg ttggacgggt gccttggaaataactaccg caacgcggcac 1020
 191 tccgcgacca cgtggagcgg ccagtcacgtc ggcggcgcgg aggcgaggat caacacccag 1080
 192 tggctctga cctccggcac caccggggcc aacgcctgga agtccacgct ggtcggccac 1140
 193 gacacccatca ccaagggtgaa ggcgtccggc gcctccatcg acgcggcgaa gaaggccggc 1200
 194 gtcaacaacg gcaaccggct cgacgcccgtt cagcgtaa 1239
 196 <210> SEQ ID NO: 6
 197 <211> LENGTH: 412
 198 <212> TYPE: PRT
 199 <213> ORGANISM: Streptomyces avidinii
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 203 1 5 10 15
 204 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
 205 20 25 30
 206 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 207 35 40 45
 208 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 209 50 55 60
 210 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 211 65 70 75 80
 212 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
 213 85 90 95
 214 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Ile Ser Gly Leu Glu Gly
 215 100 105 110

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216	Ser	Pro	Glu	Ala	Gly	Leu	Ser	Pro	Asp	Ala	Gly	Ser	Gly	Ser	Ser	Gln
217	115					120										125
218	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser
219	130					135										140
220	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Asn
221	145					150					155					160
222	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly
223						165					170					175
224	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	Lys
225						180				185						190
226	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met
227						195			200							205
228	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala
229						210			215			220				
230	Arg	Ala	Gln	Leu	Arg	Pro	Asn	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Ala
231	225					230					235					240
232	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Ser	Gly	Ser	Ala	Asp	Pro	Ser
233						245					250					255
234	Lys	Asp	Ser	Lys	Ala	Gln	Val	Ser	Ala	Ala	Glu	Ala	Gly	Ile	Thr	Gly
235						260			265			270				
236	Thr	Trp	Tyr	Asn	Gln	Leu	Gly	Ser	Thr	Phe	Ile	Val	Thr	Ala	Gly	Ala
237						275			280			285				
238	Asp	Gly	Ala	Leu	Thr	Gly	Thr	Tyr	Glu	Ser	Ala	Val	Gly	Asn	Ala	Glu
239						290			295			300				
240	Ser	Arg	Tyr	Val	Leu	Thr	Gly	Arg	Tyr	Asp	Ser	Ala	Pro	Ala	Thr	Asp
241	305					310					315					320
242	Gly	Ser	Gly	Thr	Ala	Leu	Gly	Trp	Thr	Val	Ala	Trp	Lys	Asn	Asn	Tyr
243						325					330					335
244	Arg	Asn	Ala	His	Ser	Ala	Thr	Thr	Trp	Ser	Gly	Gln	Tyr	Val	Gly	Gly
245						340					345					350
246	Ala	Glu	Ala	Arg	Ile	Asn	Thr	Gln	Trp	Leu	Leu	Thr	Ser	Gly	Thr	Thr
247						355				360			365			
248	Glu	Ala	Asn	Ala	Trp	Lys	Ser	Thr	Leu	Val	Gly	His	Asp	Thr	Phe	Thr
249						370			375			380				
250	Lys	Val	Lys	Pro	Ser	Ala	Ala	Ser	Ile	Asp	Ala	Ala	Lys	Lys	Ala	Gly
251	385					390					395					400
252	Val	Asn	Asn	Gly	Asn	Pro	Leu	Asp	Ala	Val	Gln	Gln				
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262	tgaagatgtc	ctgcaaggct	tctggctaca	catttaccag	ttacaatatg	cactgggtaa										120
263	agcagacacc	tggacagggc	ctggaaatgga	ttggagctat	ttatccagga	aatggtgata										180
264	cttcctacaa	tcagaagttc	aaaggcaagg	ccacattgac	tgcagacaaa	tcctccagca										240
265	cagcctacat	gcagctcagc	agcctgacat	ctgaggactc	tgcgggtctat	tactgtgcaa										300
266	gagcgcaatt	acgacctaac	tactggtaact	tgcgtgtctg	gggcgcagg	accacggta										360

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L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date